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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Sat May 13 09:17:00 2000; MasPar time 3.04 Seconds
124.592 Million cell updates/sec
Tabular output not generated.

Title: >US-09-331-631-27
Description: (1-16) from US09331631.pep
Perfect Score: 120
Sequence: 1 QKHRSQILGCYLXQQL 16

Scoring table: PAM 150
Gap 15

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:geneseqp

Statistics: Mean 19.307; Variance 54.468; scale 0.354

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	105	87.5	17	1	W62840	Stenocarpus sinuatus a	4.29e-05
2	64	53.3	195	1	R24944	Sequence of ovine trop	5.46e+00
3	64	53.3	195	1	R24941	Sequence of ovine trop	5.46e+00
4	64	53.3	195	1	P91396	Isoform of Class II al	5.46e+00
5	64	53.3	195	1	R24945	Sequence of ovine trop	5.46e+00
6	60	50.0	195	1	R24943	Sequence of ovine trop	1.58e+01
7	59	49.2	23	1	W62839	Stenocarpus sinuatus a	2.05e+01
8	59	49.2	135	1	Y03782	S. aureus polypeptide.	2.05e+01
9	59	49.2	377	1	R70029	Tobacco cluster-A prot	2.05e+01
10	57	47.5	195	1	R24942	Sequence of ovien trop	3.44e+01
11	57	47.5	195	1	R04540	Ovine trophoblast prot	3.44e+01
12	56	46.7	238	1	W81981	Ehrlichia sp. E82.3 pr	4.46e+01
13	55	45.8	111	1	W28096	Staphylococcus aureus	5.75e+01
14	55	45.8	222	1	Y05539	Wheat Type I glutathio	5.75e+01
15	55	45.8	396	1	W56695	Tetracycline resistanc	5.75e+01
16	55	45.8	647	1	W34535	Helicoverpa armigera v	5.75e+01
17	55	45.8	647	1	R49662	Sequence of Heliothis	5.75e+01
18	54	45.0	201	1	W20604	H. pylori cytoplasmic	7.42e+01
19	54	45.0	410	1	R10693	Cephalosporin antibiot	7.42e+01
20	54	45.0	706	1	W81353	Human hFrizzled-6 prot	7.42e+01
21	53	44.2	47	1	W20493	H. pylori secreted or	9.54e+01
22	53	44.2	86	1	W20741	H. pylori secreted or	9.54e+01
23	53	44.2	119	1	R60515	Mouse beta-2 microglob	9.54e+01
24	53	44.2	371	1	R70025	Tobacco chitinase enco	9.54e+01
25	53	44.2	1279	1	R60872	STE6-CFTR chimera H4.	9.54e+01
26	53	44.2	1279	1	R60873	STE6-CFTR chimera H5.	9.54e+01
27	52	43.3	161	1	W71485	Helicobacter polypepti	1.23e+02
28	52	43.3	195	1	R04539	cDNA clone of sequence	1.23e+02
29	52	43.3	544	1	W71203	Protein encoded by ORF	1.23e+02
30	52	43.3	802	1	R90848	Gibberellin (GA1), ent	1.23e+02
31	51	42.5	86	1	W26417	Swinepox virus HindIII	1.57e+02
32	51	42.5	331	1	W29817	Mammalian AMPK-gamma s	1.57e+02
33	51	42.5	349	1	W06416	Phosphotriesterase-rel	1.57e+02
34	51	42.5	725	1	W80363	The large subunit (R1)	1.57e+02
35	50	41.7	47	1	Y03000	Fragment of human secr	2.01e+02
36	50	41.7	72	1	Y02999	Fragment of human secr	2.01e+02
37	50	41.7	553	1	W10691	Newcastle disease viru	2.01e+02
38	50	41.7	553	1	W06828	Newcastle disease viru	2.01e+02
39	50	41.7	553	1	R49141	Newcastle disease viru	2.01e+02
40	50	41.7	572	1	W31273	Mouse frizzled-7 prote	2.01e+02
41	50	41.7	585	1	W31271	Human frizzled-5 prote	2.01e+02
42	50	41.7	666	1	W31268	Mouse frizzled-3 prote	2.01e+02
43	50	41.7	758	1	W97677	Human KDS2 protein kin	2.01e+02
44	50	41.7	1311	1	W72971	Precis coenia patched	2.01e+02
45	50	41.7	1311	1	W52197	Precis coenia (butterf	2.01e+02

ALIGNMENTS

RESULT 1
ID W62840 standard; Protein; 17 AA.
AC W62840;
DT 27-OCT-1998 (first entry)
DE Stenocarpus sinuatus antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Stenocarpus sinuatus.
FH Key Location/Qualifiers
FT Misc_difference 13
FT /note= "uhdefined amino acid"
PN WO9827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI; 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 66; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 17 AA;

Query Match 87.5%; Score 105; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.29e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 QKHRSQILGCYLXCQQL 17
||||||||||||| |||
Qy 1 QKHRSQILGCYLX-QQL 16

RESULT 2
ID R24944 standard; Protein; 195 AA.
AC R24944;
DT 03-JAN-1992 (first entry)
DE Sequence of ovine trophoblastin variant Xc.
KW Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW trophoblastin; antiluteolytic agent.
OS Ammotragus lervia.
FH Key Location/Qualifiers
FT peptide 1. .23
FT /label= signal
PN WO9209691-A.
PD 11-JUN-1992.

PF 29-NOV-1991; F00953.
PR 29-NOV-1990; FR-014945.
PR 29-NOV-1990; FR-014946.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (TRGE) TRANSGENE SA.
PI Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,
PI Martal J, Reinaud P;
DR WPI; 92-217070/26.
PT New type I interferon variants with added N-terminal di:peptide -
PT include expression cassettes providing high yield in yeast, esp.
PT trophoblast derivs. with e.g. anti-luteolytic activity
PS Claim 7; page 30; 53pp; French.
CC The DNA sequence encoding the precursor of ovine trophoblastin was
CC disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are
CC isoforms of trophoblastin. They have anti-luteolytic activity and
CC are used to improve survival of transplanted embryos; as a reagent
CC for detecting viability of embryos at an early stage of its
CC development; and to improve the fertility of livestock.
SQ Sequence 195 AA;

Query Match 53.3%; Score 64; DB 1; Length 195;
Best Local Similarity 77.8%; Pred. No. 5.46e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 22 LGCYLSQRL 30
|||||.|:|
Qy 8 LGCYLXQQL 16

RESULT 3
ID R24941 standard; Protein; 195 AA.
AC R24941;
DT 03-JAN-1992 (first entry)
DE Sequence of ovine trophoblastin.
KW Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW trophoblastin; antiluteolytic agent.
OS Ammotragus lervia.
FH Key Location/Qualifiers
FT peptide 1. .23
FT /label= signal
PN WO9209691-A.
PD 11-JUN-1992.
PF 29-NOV-1991; F00953.
PR 29-NOV-1990; FR-014945.
PR 29-NOV-1990; FR-014946.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (TRGE) TRANSGENE SA.
PI Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,
PI Martal J, Reinaud P;
DR WPI; 92-217070/26.
PT New type I interferon variants with added N-terminal di:peptide -
PT include expression cassettes providing high yield in yeast, esp.
PT trophoblast derivs. with e.g. anti-luteolytic activity
PS Disclosure; Fig 1; 53pp; French.
CC The DNA sequence encoding the precursor of ovine trophoblastin was
CC disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are
CC isoforms of trophoblastin. They have anti-luteolytic activity and
CC are used to improve survival of transplanted embryos; as a reagent
CC for detecting viability of embryos at an early stage of its
CC development; and to improve the fertility of livestock.
SQ Sequence 195 AA;

Query Match 53.3%; Score 64; DB 1; Length 195;
Best Local Similarity 77.8%; Pred. No. 5.46e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 22 LGCYLSQRL 30
|||||.|:|
Qy 8 LGCYLXQQL 16

RESULT 4
ID P91396 standard; protein; 195 AA.
AC P91396;
DT 15-FEB-1990 (first entry)
DE Isoform of Class II alpha-interferon trophoblastine precursor.
KW Antiviral; antitumour.
PN WO8908706-A.
PD 21-SEP-1989.
PF 17-MAR-1989; F00116.
PR 18-MAR-1988; FR-003591.
PA (INRG) Inst Nat Rech Agron.
PI Martal J, Charpigny G, Gaye P, Pernollet J, Charlier M, Guillomot M,
PI Huet J, Reinaud P, Hue D, Chene N, La Bonnardiere C;
DR WPI; 89-292521/40.
PT New isoform(s) of the class II alpha interferon trophoblastine
PT - with eg antiviral, antitumour and immuno-modulating activities, and
PT new DNA encoding sequences.
PS Claim 11; page 11; 47pp; French.
CC The isoform (23 kD) can be used for immunological, rejection-inhibiting,
CC and cell differentiation activities. It can inhibit luteolysis at the
CC start of pregnancy, monitor embryo viability, and protect embryos during
CC transfer to the womb of a recipient.
SQ Sequence 195 AA;

Query Match 53.3%; Score 64; DB 1; Length 195;
Best Local Similarity 77.8%; Pred. No. 5.46e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 22 LGCYLSQRL 30
|||||.|:|
Qy 8 LGCYLXQQL 16

RESULT 5
ID R24945 standard; Protein; 195 AA.
AC R24945;
DT 03-JAN-1992 (first entry)
DE Sequence of ovine trophoblastin variant Xd.
KW Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW trophoblastin; antiluteolytic agent.
OS Ammotragus lervia.
FH Key Location/Qualifiers
FT peptide 1. .23
FT /label= signal
PN WO9209691-A.
PD 11-JUN-1992.
PF 29-NOV-1991; F00953.
PR 29-NOV-1990; FR-014945.
PR 29-NOV-1990; FR-014946.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (TRGE) TRANSGENE SA.
PI Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,
PI Martal J, Reinaud P;
DR WPI; 92-217070/26.
PT New type I interferon variants with added N-terminal di:peptide -
PT include expression cassettes providing high yield in yeast, esp.
PT trophoblast derivs. with e.g. anti-luteolytic activity
PS Claim 7; page 30; 53pp; French.
CC The DNA sequence encoding the precursor of ovine trophoblastin was
CC disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are
CC isoforms of trophoblastin. They have anti-luteolytic activity and
CC are used to improve survival of transplanted embryos; as a reagent
CC for detecting viability of embryos at an early stage of its
CC development; and to improve the fertility of livestock.
SQ Sequence 195 AA;

Query Match 53.3%; Score 64; DB 1; Length 195;
Best Local Similarity 77.8%; Pred. No. 5.46e+00;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 22 LGCYLSQRL 30
|||||.|:|
Qy 8 LGCYLXQQL 16

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RESULT    6
ID   R24943 standard; Protein; 195 AA.
AC   R24943;
DT   03-JAN-1992  (first entry)
DE   Sequence of ovine trophoblastin variant Xb
KW   Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW   trophoblastin; antiluteolytic agent.
OS   Ammotragus lervia.
FH   Key             Location/Qualifiers
FT   peptide         1. .23
FT                   /label= signal
PN   WO9209691-A.
PD   11-JUN-1992.
PF   29-NOV-1991; F00953.
PR   29-NOV-1990; FR-014945.
PR   29-NOV-1990; FR-014946.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA   (TRGE ) TRANSGENE SA.
PI   Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,
PI   Martal J, Reinaud P;
DR   WPI; 92-217070/26.
PT   New type I interferon variants with added N-terminal di:peptide -
PT   include expression cassettes providing high yield in yeast, esp.
PT   trophoblast derivs. with e.g. anti-luteolytic activity
PS   Claim 7; page 30; 53pp; French.
CC   The DNA sequence encoding the precursor of ovine trophoblastin was
CC   disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are
CC   isoforms of trophoblastin.  They have anti-luteolytic activity and
CC   are used to improve survival of transplanted embryos; as a reagent
CC   for detecting viability of embryos at an early stage of its
CC   development; and to improve the fertility of livestock.
SQ   Sequence   195 AA;

  Query Match           50.0%;  Score 60;  DB 1;  Length 195;
  Best Local Similarity  66.7%;  Pred. No. 1.58e+01;
  Matches     6;  Conservative    2;  Mismatches   1;  Indels   0;  Gaps   0;

Db     22 LGCYLSERL 30
          ||||| ::|
Qy      8 LGCYLXQQL 16


RESULT    7
ID   W62839 standard; Protein; 23 AA.
AC   W62839;
DT   27-OCT-1998  (first entry)
DE   Stenocarpus sinuatus antimicrobial protein.
KW   antimicrobial protein; infestation; control.
OS   Stenocarpus sinuatus.
PN   WO9827805-A1.
PD   02-JUL-1998.
PF   22-DEC-1997; AU0874.
PR   20-DEC-1996; AU-004275.
PA   (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI   Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR   WPI; 98-377279/32.
PT   Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT   useful for controlling microbial infestations of plants or mammals
PS   Claim 1; Page 65; 96pp; English.
CC   The sequence is that of an antimicrobial protein which can
CC   be used to control microbial infestations in plants and mammalian
CC   animals.
SQ   Sequence   23 AA;

  Query Match           49.2%;  Score 59;  DB 1;  Length 23;
  Best Local Similarity  61.5%;  Pred. No. 2.05e+01;
  Matches     8;  Conservative    2;  Mismatches   2;  Indels   1;  Gaps   1;

Db     10 RGEILECYRLCQQ 22
          |::|| || | ||
Qy      4 RSQILGCY-LXQQ 15


RESULT    8
ID   Y03782 standard; Protein; 135 AA.
AC   Y03782;
DT   11-JUN-1999  (first entry)
DE   S. aureus polypeptide.
KW   Staphylococcus aureus polypeptide; thyroiditis; infective carditis;
KW   lung abscess; secretory diarrhoea; cerebral abscess; conjunctivitis;
KW   toxic shock syndrome; folliculitis; septic arthritis; antibacterial;
KW   H pylori infection; gastric ulcer; adenocarcinoma.
OS   Staphylococcus aureus.
PN   EP-905243-A2.
PD   31-MAR-1999.
PF   03-AUG-1998; 306185.
PR   05-AUG-1997; US-055387.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PI   Burnham MKR, Lonetto MA, Warren PV;
DR   WPI; 99-192667/17.
DR   N-PSDB; X31852.
PT   New essential polypeptides from Staphylococcus aureus useful for
PT   treating diseases such as infective endocarditis and toxic shock
PT   syndrome
PS   Claim 11; Page 24-25; 70pp; English.
CC   The invention provides new Staphylococcus aureus polypeptides (Y03781-94)
CC   and the genes (X31851-864) encoding them. Host cells containing vectors
CC   comprising the nucleic acid sequences are used for the recombinant
CC   expression of the proteins. The polypeptides can be used to screen for
CC   modulators for use in antibacterial therapy. The polypeptides, their
CC   antagonists and agonists are used to prevent or treat diseases caused by
CC   S. aureus such as thyroiditis, lung abscesses,. infective carditis,
CC   secretory diarrhoea, cerebral abscesses, conjunctivitis, toxic shock
CC   syndrome folliculitis and septic arthritis. Screening for the presence of
CC   the polypeptides may be used to diagnose, predict the susceptibility to,
CC   or stage the progress of these S. aureus diseases and diseases caused by
CC   Helicobacter pylori such as gastric ulcers and gastric adenocarcinoma.
CC   There is not much information known about the essential genes expressed
CC   by S. aureus during infection but these new polypeptides have been
CC   identified as essential. They can therefore be used to develop
CC   antibacterial compounds specific for those essential genes and this
CC   ensures the effectiveness of the compounds in killing S. aureus. In
CC   addition, these polypeptides can be used to effectively diagnose and
CC   treat infections and diseases caused by S. aureus without the risk of
CC   development of antibiotic resistance. The present sequence represents a
CC   S. aureus polypeptide which has homology to a B. subtilis probable
CC   acetyltransferase.
SQ   Sequence   135 AA;

  Query Match           49.2%;  Score 59;  DB 1;  Length 135;
  Best Local Similarity  43.8%;  Pred. No. 2.05e+01;
  Matches     7;  Conservative    3;  Mismatches   6;  Indels   0;  Gaps   0;

Db     42 HMHRKTSLGYYLYKQF 57
          ::||   || ||  |:
Qy      1 QKHRSQILGCYLXQQL 16


RESULT    9
ID   R70029 standard; Protein; 377 AA.
AC   R70029;
DT   29-SEP-1995  (first entry)
DE   Tobacco cluster-A protein encoded by genomic clone.
KW   Tobacco; chitinase; antifungal; fungicide; Cluster-A.
OS   Nicotiana tabacum.
FH   Key             Location/Qualifiers
FT   peptide         1. .25
FT                   /label= signal peptide
FT   misc_difference 28. .29
FT                   /note= "cDNA encodes additional Ile here"
FT   misc_difference 188. .201
FT                   /label= Determined by sequencing the protein
FT   misc_difference 222. .247
FT                   /note= "Determined by sequencing the protein"
PN   EP-639642-A.
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PD   22-FEB-1995.
PF   17-AUG-1993; 202425.
PR   17-AUG-1993; EP-202425.
PA   (MOGE-) MOGEN INT NV.
PA   (UYLE-) RIJKSUNIV LEIDEN.
PI   Apotheker-de Groot M,  Bol JF,  Cornelissen BJC,  Linthorst HJM;
PI   Melchers LS,  Ponstein AS,  Sela-buurlage MB;
DR   WPI; 95-083454/12.
DR   N-PSDB; Q82976.
PT   New plant protein having endo-chitinase activity - used in
PT   antifungal compsns. and to develop transformed plants which are
PT   less susceptible to fungal infection.
PS   Claim 3; Page 25-28; 43pp; English.
CC   Screening of a lambda ZAP cDNA library of TMV-infected Samsunn NN
CC   tobacco plants with a probe derived from PROB40 (a partial Cluster-A
CC   cDNA clone) resulted in the isolated of 11 positively hybridising
CC   clones. Analysis revealed that all were identical and corresp. to
CC   Cluster-A cDNA.The sequence of cDNA clone cA-3 is given in Q82973/
CC   R70025. A genomic library of N. tabacum was screened using the
CC   Cluster-A cDNA insert of clone cA-3 as a probe (see Q82977, Q82978).
CC   The complete nt. sequence of Cluster-A cDNA including the deduced
CC   primary structure of the Cluster-A protein the 5' and 3' UTR regions
CC   of the gene are shown in Q82976/R70029. Comaprison of the cDNA
CC   clone with the Cluster-A gene revealed that these sequences share
CC   a high degree of identity (94%). The Cluster-A precursor protien
CC   contains a putative signal peptide as well as 4 potential N-linked
CC   glycosylation sites (N-X-S/T). The predicted mature protein has
CC   a calculated mol. wt. of 39,033 Da.
SQ   Sequence   377 AA;

  Query Match           49.2%;  Score 59;  DB 1;  Length 377;
  Best Local Similarity  60.0%;  Pred. No. 2.05e+01;
  Matches     6;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db     11 IFSCFLLQQL 20
          |::|:| |||
Qy      7 ILGCYLXQQL 16


RESULT   10
ID   R24942 standard; Protein; 195 AA.
AC   R24942;
DT   03-JAN-1992  (first entry)
DE   Sequence of ovien trophoblastin variant Xa.
KW   Antiviral; antiinflammatory; antitumour; immunomodulator; immunogen;
KW   trophoblastin; antiluteolytic agent.
OS   Ammotragus lervia.
FH   Key             Location/Qualifiers
FT   peptide         1. .23
FT                   /label= signal
PN   WO9209691-A.
PD   11-JUN-1992.
PF   29-NOV-1991; F00953.
PR   29-NOV-1990; FR-014945.
PR   29-NOV-1990; FR-014946.
PA   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
PA   (TRGE ) TRANSGENE SA.
PI   Degryse E, Chaouat G, Charlier M, Charpigny G, Gaye P,
PI   Martal J, Reinaud P;
DR   WPI; 92-217070/26.
PT   New type I interferon variants with added N-terminal di:peptide -
PT   include expression cassettes providing high yield in yeast, esp.
PT   trophoblast derivs. with e.g. anti-luteolytic activity
PS   Claim 7; page 30; 53pp; French.
CC   The DNA sequence encoding the precursor of ovine trophoblastin was
CC   disclosed in PCT WO 89/08706 (see R24941). R24942-R24945 are
CC   isoforms of trophoblastin.  They have anti-luteolytic activity and
CC   are used to improve survival of transplanted embryos; as a reagent
CC   for detecting viability of embryos at an early stage of its
CC   development; and to improve the fertility of livestock.
SQ   Sequence   195 AA;

  Query Match           47.5%;  Score 57;  DB 1;  Length 195;
  Best Local Similarity  66.7%;  Pred. No. 3.44e+01;
  Matches     6;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db     22 LGCYLSRKL 30
          ||||| : |
Qy      8 LGCYLXQQL 16


RESULT   11
ID   R04540 standard; protein; 195 AA.
AC   R04540;
DT   17-SEP-1990  (first entry)
DE   Ovine trophoblast protein-1 (oTP-1).
KW   Bovine trophoblast protein-1; bTP-1; fertility; ds.
OS   Sus scrofa.
PN   EP-367063-A.
PD   9-MAY-1990.
PF   23-OCT-1989; 119642.
PR   26-OCT-1988; US-262870.
PA   (UMOR) Univ of Missouri.
PI   Roberts MR, Imakawa K;
DR   WPI; 90-141062/19.
DR   N-PSDB; Q04289
PT   Recombinant bovine trophoblast protein-1 -
PT   used for enhancing fertility or treating viral diseases in
PT   mammals, esp. cattle.
PS   Disclosure; p; English.
CC   The bTP-1 produced from the gene may be used to promote fertility
CC   or treat viral disease in cattle. The gene may also be used to
CC   provide transgenic animals with enhanced fertility, or in
CC   prophylactic and therapuetic treatment of other mammals.
SQ   Sequence   195 AA;

  Query Match           47.5%;  Score 57;  DB 1;  Length 195;
  Best Local Similarity  66.7%;  Pred. No. 3.44e+01;
  Matches     6;  Conservative    1;  Mismatches   2;  Indels   0;  Gaps   0;

Db     22 LGCYLSRKL 30
          ||||| : |
Qy      8 LGCYLXQQL 16


RESULT   12
ID   W81981 standard; Protein; 238 AA.
AC   W81981;
DT   02-MAR-1999  (first entry)
DE   Ehrlichia sp. E82.3 protein.
KW   Granulocytic ehrlichia; GE; E82; tick-borne infection; fatal; vaccine;
KW   immune response; detection; diagnosis; Ehrlichiosis.
OS   Ehrlichia sp.
PN   WO9849312-A2.
PD   05-NOV-1998.
PF   24-APR-1998; U08264.
PR   25-APR-1997; US-044869.
PA   (AQUI-) AQUILA BIOPHARMACEUTICALS INC.
PI   Beltz G, Coughlin RT, Murphy C, Storey J;
DR   WPI; 99-034663/03.
DR   N-PSDB; V65142.
PT   New isolated granulcytic erhlichia nucleic acids - used to develop
PT   products for use in vaccines for inhibiting Ehrlichiosis and for use
PT   in detection and diagnosis
PS   Claim 1a; Fig 10; 184pp; English.
CC   This sequence encodes the E82.3 protein which is associated with and has
CC   been isolated from HL60 cells infected with Ehrlichia sp. GE is an acute
CC   potentially fatal tick borne infection and the proteins described in
CC   this invention can be used in vaccines to elicit a beneficial immune
CC   response in an animal to GE. They can be used for inhibiting Ehrlichoisis
CC   in an animal. The products can also be used for detection and diagnosis.
SQ   Sequence   238 AA;

  Query Match           46.7%;  Score 56;  DB 1;  Length 238;
  Best Local Similarity  54.5%;  Pred. No. 4.46e+01;
  Matches     6;  Conservative    3;  Mismatches   2;  Indels   0;  Gaps   0;
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Db    204 QILGYFLHRHL 214
          |||| :| ::|
Qy      6 QILGCYLXQQL 16
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RESULT   13
ID   W28096 standard; Protein; 111 AA.
AC   W28096;
DT   01-SEP-1998  (first entry)
DE   Staphylococcus aureus protein of unknown function.
KW   Staphylococcus aureus protein; ribozyme; antisense sequence; control;
KW   Staphylococcal gene; regulatory element; bacterial gene expression;
KW   vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
KW   toxic shock syndrome.
OS   Staphylococcus aureus.
FH   Key             Location/Qualifiers
FT   Misc_difference 1. .111
FT                   /note= "residues designated X are not defined in
FT                          the specification"
PN   WO9730070-A1.
PD   21-AUG-1997.
PF   19-FEB-1997; U02318.
PR   20-FEB-1996; US-011888.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PI   Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
PI   Pratt JM, Reichard RW, Rosenberg M, Ward JM;
DR   WPI; 97-424969/39.
DR   N-PSDB; T84032.
PT   Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used
PT   to isolate antimicrobial compounds, and in vaccines against S.
PT   aureus infection
PS   Claim 6; Page 463; 989pp; English.
CC   The present sequence represents a Staphylococcus aureus protein of
CC   unknown function. The DNA sequence was isolated from a library of
CC   clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can
CC   be used in the construction of ribozymes and antisense sequences to
CC   control the expression of Staphylococcal genes. The DNA sequence is
CC   also useful as a source of regulatory elements for the control of
CC   bacterial gene expression. The present protein may be used to produce
CC   vaccines to enable a host to produce specific antibodies with
CC   antibacterial action. These vaccines and antibodies would protect
CC   a host against invasion by S. aureus, and conditions relating to
CC   Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled
CC   skin syndrome, and toxic shock syndrome.
SQ   Sequence   111 AA;

  Query Match           45.8%;  Score 55;  DB 1;  Length 111;
  Best Local Similarity  85.7%;  Pred  No. 5.75e+01;
  Matches     6;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db      7 CYLKQQL 13
          ||| |||
Qy     10 CYLXQQL 16
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RESULT   14
ID   Y05539 standard; Protein; 222 AA.
AC   Y05539;
DT   05-JUL-1999  (first entry)
DE   Wheat Type I glutathione transferase subunit IC2.
KW   Glutathione transferase; GST; glutathione peroxidase; wheat; WIC2;
KW   IC2; herbicide resistance; transgenic plant.
OS   Triticum aestivum.
PN   WO9914337-A2.
PD   25-MAR-1999.
PF   16-SEP-1998; G02802.
PR   16-SEP-1997; GB-019727.
PA   (RHON ) RHONE-POULENC AGRIC LTD.
PI   Cole DJ, Cummins I, Edwards R;
DR   WPI; 99-244035/20.
DR   N-PSDB; X25146.
PT   New isolated glutathione transferase subunit polynucleotides
PS   Claim 3; Page 83; 101pp; English.
CC   The present sequence represents IC2, a wheat glutathione transferase
CC   (GST) subunit that resembles the type I GSTs from maize.  Clone
CC   WIC2 (see X25146), which codes for IC2, was isolated from a cDNA
CC   expression library prepared from fenchlorazole-ethyl (herbicide
CC   safener) treated wheat shoots using maize GST antiserum.
CC   Recombinant IC2 shows activity toward herbicides and non-herbicide
CC   substrates, and also has glutathione peroxidase activity toward
CC   organic hydroperoxides.  The invention provides cDNAs and genomic
CC   DNAs (see X25144-52) encoding wheat GST subunits (see Y05537-45)
CC   active in herbicide metabolism.  This is fundamental to
CC   understanding GST detoxification in wheat and in the development
CC   of transgenic herbicide resistant plants expressing wheat GSTs.
CC   The invention also provides methods of identifying compounds
CC   capable of metabolism by GST, or compounds that induce GST
CC   expression in graminaceous plants, and for determining the GST
CC   level in a sample of seed or flour.  Transgenic plants, host cells
CC   used for production of GST subunits and GST dimeric proteins, and
CC   vectors are also provided.
SQ   Sequence   222 AA;

  Query Match           45.8%;  Score 55;  DB 1;  Length 222;
  Best Local Similarity  50.0%;  Pred. No. 5.75e+01;
  Matches     5;  Conservative    5;  Mismatches   0;  Indels   0;  Gaps   0;

Db     78 RKHKPELLGC 87
          :||::::|||
Qy      1 QKHRSQILGC 10
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RESULT   15
ID   W56695 standard; Protein; 396 AA.
AC   W56695;
DT   24-JUL-1998  (first entry)
DE   Tetracycline resistance sequence contained in plasmid pRZTL1 .
KW   Tn5 transposase; modified; enzyme; in vitro transposition; mutant;
KW   target; marker; transposon 5; plasmid pRZTL1; tetracycline resistance.
OS   Synthetic.
OS   Escherichia coli.
PN   WO9810077-A1.
PD   12-MAR-1998.
PF   09-SEP-1997; U15941.
PR   02-MAY-1997; US-850880.
PR   09-SEP-1996; US-814877.
PA   (WISC ) WISCONSIN ALUMNI RES FOUND.
PI   Goryshin IY, Reznikoff WS, Zhou H;
DR   WPI; 98-193627/17.
DR   N-PSDB; V28398.
PT   Modified Tn5 transposase construct used in novel system for in vitro
PT   transposition - used to, e.g. create absolute defective mutants,
PT   provide selective markers and to facilitate insertion of specialised
PT   DNA sequences into target DNA
PS   Disclosure; Pages 35-46; 73pp; English.
CC   This tetracycline resistance sequence is contained in the plasmid
CC   pRZTL1 which is used to demonstrate in vitro transposition of a
CC   transposable element located between a pair of Tn5 (transposon 5)
CC   outside end (OE) termini. The invention provides a genetic construct
CC   that contains a nucleotide sequence encoding a modified Tn5 transposase
CC   enzyme that has both greater avidity for Tn5 OE repeats and is less
CC   likely to assume an inactive multimeric form than a wild type Tn5
CC   transposase and a transposable DNA sequence flanked at its 5' and 3' ends
CC   by an 18 or 19 base pair flanking DNA sequence comprising nucleotide A
CC   at position 10, T at 11 and A at 12. The modified Tn5 transposase and
CC   the transposable DNA which is a DNA donor molecule are used in a system
CC   for in vitro transposition. The system and method can be used to create
CC   absolute defective mutants, to provide selective markers to target DNA,
CC   to provide portable regions of homology to a target DNA, to facilitate
CC   insertion of specialised DNA sequences into target DNA, to provide primer
CC   binding sites or tags for DNA sequencing , to facilitate production of
CC   genetic fusion for gene expression studies and protein domain mapping, as
CC   well as to bring together other desired combinations of DNA sequences
CC   (combinatorial genetics). The modified Tn5 transposase facilitates in
CC   vitro transposition reaction rates of at least about 100-fold higher
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CC   than can be achieved using wild type transposase (as measure in vivo).
CC   In vitro transposition using this system can also use donor DNA and
CC   target DNA that is circular or linear. The system also requires no
CC   outside high energy source and no other protein other than the modified
CC   transposase.
SQ   Sequence   396 AA;

  Query Match           45.8%;  Score 55;  DB 1;  Length 396;
  Best Local Similarity  55.6%;  Pred. No. 5.75e+01;
  Matches     5;  Conservative    3;  Mismatches   1;  Indels   0;  Gaps   0;

Db    175 LLGCFLMQE 183
          :|||:| |:
Qy      7 ILGCYLXQQ 15


Search completed: Sat May 13 09:17:07 2000
Job time : 7 secs.
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